

Angell, Jon E

From: Angell, Jon E
Sent: Friday, September 01, 2006 2:37 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search Request 10/674,836

Sequence Search Request 10/674,836

Examiner# : 78697
Art Unit : 1635
Phone Number: 571-272-0756
Mailbox & Bldg/Room Location: REMSEN 2C18
Results Format Preferred (circle): DISK

I would like to have a standard search performed using the following :

- 1) nucleotides 13306 through 13509 of SEQ ID NO:1
- 2) nucleotides 13428 through 13509 of SEQ ID NO:1

In addition to the standard search of #1 and #2 above, please include searches for #2 (13428-13509 of SEQ ID NO:1) that only return hits that are A) 400-900 nucleotides in length, B) 200-400 nucleotides in length, and c) 100-200 nucleotides in length.

Please contact me by phone or email if you have any questions.

Thanks,
Eric

J. Eric Angell
Art Unit 1635
Office: REMSEN 2D20
mailbox: REM 2C18
571-272-0756

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2006, 17:23:08 ; Search time 5278.32 Seconds
 (without alignments)
 2161.207 Million cell updates/sec

Title: US-10-674-836-1_COPY_13306_13509
 Perfect score: 204
 Sequence: 1 gtggcggagggaactggggac.....gcagcgctgcgtcctgctgc 204

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
c	1	70.6	34.6	666	13	CW946150	CW946150 TcB28.4_B
c	2	70.6	34.6	855	1	AL573255	AL573255 AL573255
c	3	69.2	33.9	890	13	CL493826	CL493826 SAIL_586_
	4	69	33.8	1081	13	CL464716	CL464716 SAIL_1225
	5	69	33.8	1328	14	AG320910	AG320910 Mus muscu
	6	68.6	33.6	934	13	CL477947	CL477947 SAIL_283_

	7	68.4	33.5	572	11	BZ050840	BZ050840 jnr64d12.
c	8	68.4	33.5	1806	12	CG756794	CG756794 P051-4-G0
	9	68.2	33.4	675	11	BZ050815	BZ050815 jnr64a12.
	10	67.2	32.9	458	14	CNS00D2T	AL060559 Drosophil
c	11	67.2	32.9	916	3	BU197009	BU197009 AGENCOURT
	12	67.2	32.9	1051	4	CB206210	CB206210 AGENCOURT
c	13	67	32.8	566	14	CNS03JN0	AL247077 Tetraodon
	14	67	32.8	898	5	CK414740	CK414740 AUF_IpGil
c	15	67	32.8	1330	12	CL063297	CL063297 CH216-99P
c	16	67	32.8	1675	14	AG360980	AG360980 Mus muscu
	17	66.6	32.6	579	14	CNS04OTC	AL300441 Tetraodon
	18	66.6	32.6	921	13	CL489959	CL489959 SAIL_531_
	19	66.6	32.6	949	13	CL465953	CL465953 SAIL_1249
	20	66.6	32.6	969	13	CL477043	CL477043 SAIL_267_
c	21	66.6	32.6	988	3	BU183975	BU183975 AGENCOURT
	22	66.6	32.6	1374	14	AG435756	AG435756 Mus muscu
	23	66.6	32.6	1695	12	CC290874	CC290874 CH261-172
c	24	66.4	32.5	822	14	AG430981	AG430981 Mus muscu
	25	66.4	32.5	1040	13	CL466687	CL466687 SAIL_125_
c	26	66.2	32.5	881	4	BX427015	BX427015 BX427015
c	27	66.2	32.5	897	13	CL470675	CL470675 SAIL_146_
c	28	66.2	32.5	933	14	CNS006XG	AL066047 Drosophil
	29	66.2	32.5	1026	3	BU900073	BU900073 AGENCOURT
	30	66.2	32.5	1128	3	BU841360	BU841360 AGENCOURT
	31	66	32.4	774	14	AG479706	AG479706 Mus muscu
c	32	66	32.4	1066	4	CB905393	CB905393 tric074xd
c	33	66	32.4	1066	5	CF876920	CF876920 tric074xd
c	34	65.8	32.3	675	14	CR152762	CR152762 Reverse s
c	35	65.8	32.3	902	2	BI956545	BI956545 HVSMEn000
	36	65.8	32.3	1008	3	BQ942600	BQ942600 AGENCOURT
	37	65.8	32.3	1109	13	CL515456	CL515456 SAIL_8_E1
c	38	65.8	32.3	1289	12	CL147104	CL147104 ISB1-156E
c	39	65.8	32.3	1622	13	CL476695	CL476695 SAIL_258_
c	40	65.8	32.3	1691	14	AG341104	AG341104 Mus muscu
c	41	65.6	32.2	881	9	DN565434	DN565434 91010253
c	42	65.6	32.2	957	3	BQ423706	BQ423706 AGENCOURT
	43	65.6	32.2	988	13	CL477397	CL477397 SAIL_272_
c	44	65.4	32.1	792	14	AG449674	AG449674 Mus muscu
c	45	65.4	32.1	856	2	BI952342	BI952342 HVSMEm000

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2006, 17:48:56 ; Search time 127 Seconds
(without alignments)
1064.709 Million cell updates/sec

Title: US-10-674-836-1_COPY_13428_13509
Perfect score: 82
Sequence: 1 ccctcccagcccctcccctt.....gcagcgctgcgtcctgctgc 82

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2281053 seqs, 824500224 residues

Total number of hits satisfying chosen parameters: 206322

Minimum DB seq length: 200

Maximum DB seq length: 400

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	77.8	94.9		314	7	US-11-416-160-8	Sequence 8, Appli
2	30.6	37.3		201	6	US-10-284-444-25832	Sequence 25832, A
c 3	25.6	31.2		379	8	US-11-266-748A-177592	Sequence 177592,
4	25.6	31.2		379	8	US-11-266-748A-248086	Sequence 248086,
5	25.6	31.2		393	8	US-11-266-748A-256733	Sequence 256733,
c 6	25.6	31.2		393	8	US-11-266-748A-317250	Sequence 317250,
7	25.4	31.0		219	8	US-11-301-554-1124	Sequence 1124, Ap
c 8	25.4	31.0		294	8	US-11-301-554-1199	Sequence 1199, Ap
c 9	24.4	29.8		383	8	US-11-266-748A-37162	Sequence 37162, A
c 10	24.4	29.8		398	8	US-11-266-748A-85337	Sequence 85337, A
11	24.4	29.8		398	8	US-11-266-748A-138148	Sequence 138148,
c 12	24.2	29.5		315	8	US-11-266-748A-249652	Sequence 249652,

	13	23.8	29.0	262	8	US-11-266-748A-75445	Sequence 75445, A
	14	23.8	29.0	262	8	US-11-266-748A-108903	Sequence 108903,
c	15	23.8	29.0	262	8	US-11-266-748A-128256	Sequence 128256,
c	16	23.8	29.0	287	8	US-11-266-748A-410144	Sequence 410144,
c	17	23.6	28.8	201	6	US-10-284-444-35034	Sequence 35034, A
	18	23.6	28.8	285	8	US-11-266-748A-100971	Sequence 100971,
c	19	23.6	28.8	285	8	US-11-266-748A-153782	Sequence 153782,
	20	23.6	28.8	303	8	US-11-266-748A-358392	Sequence 358392,
c	21	23.6	28.8	303	8	US-11-266-748A-441771	Sequence 441771,
	22	23.6	28.8	313	8	US-11-266-748A-4261	Sequence 4261, Ap
	23	23.6	28.8	365	8	US-11-266-748A-94534	Sequence 94534, A
c	24	23.6	28.8	365	8	US-11-266-748A-147345	Sequence 147345,
	25	23.6	28.8	380	8	US-11-266-748A-33852	Sequence 33852, A
c	26	23.4	28.5	239	8	US-11-266-748A-410551	Sequence 410551,
	27	23.4	28.5	294	8	US-11-266-748A-410156	Sequence 410156,
c	28	23.4	28.5	390	6	US-10-374-780A-1629	Sequence 1629, Ap
c	29	23.2	28.3	201	6	US-10-284-444-31621	Sequence 31621, A
c	30	23.2	28.3	384	8	US-11-266-748A-353381	Sequence 353381,
	31	23.2	28.3	384	8	US-11-266-748A-436760	Sequence 436760,
	32	23	28.0	353	8	US-11-266-748A-37533	Sequence 37533, A
	33	23	28.0	385	8	US-11-266-748A-250338	Sequence 250338,
	34	23	28.0	385	8	US-11-266-748A-274932	Sequence 274932,
c	35	23	28.0	385	8	US-11-266-748A-310855	Sequence 310855,
	36	22.8	27.8	201	6	US-10-284-444-34669	Sequence 34669, A
c	37	22.8	27.8	328	8	US-11-266-748A-296551	Sequence 296551,
c	38	22.6	27.6	338	8	US-11-266-748A-82659	Sequence 82659, A
c	39	22.6	27.6	338	8	US-11-266-748A-111385	Sequence 111385,
	40	22.6	27.6	338	8	US-11-266-748A-135470	Sequence 135470,
	41	22.6	27.6	389	6	US-10-953-349-31775	Sequence 31775, A
	42	22.4	27.3	201	6	US-10-284-444-35227	Sequence 35227, A
c	43	22.4	27.3	238	8	US-11-266-748A-355222	Sequence 355222,
c	44	22.4	27.3	238	8	US-11-266-748A-385212	Sequence 385212,
	45	22.4	27.3	238	8	US-11-266-748A-438601	Sequence 438601,

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2006, 17:23:08 ; Search time 2121.68 Seconds
(without alignments)
2161.207 Million cell updates/sec

Title: US-10-674-836-1_COPY_13428_13509
Perfect score: 82
Sequence: 1 ccctcccagcccctcccctt.....gcagcgctgcgtcctgctgc 82

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
c	1	36.2	44.1	1352	7	BE880315		BE880315	601490686
	2	36	43.9	935	2	BG863518		BG863518	602798802
	3	34.6	42.2	1278	5	CK232592		CK232592	ILLUMIGEN
	4	34.2	41.7	1283	13	CL509378		CL509378	SAIL_811
	5	34	41.5	1008	14	AG149215		AG149215	Pan trogl
	6	33.8	41.2	1151	3	BM927078		BM927078	AGENCOURT
c	7	33.6	41.0	463	5	CJ132427		CJ132427	CJ132427
c	8	33.6	41.0	999	14	AG387695		AG387695	Mus muscu

	9	33.4	40.7	409	8	CN274427	CN274427 170005313
c	10	33.4	40.7	1253	9	DN430435	DN430435 LIB4217-0
c	11	33.2	40.5	717	13	CZ666881	CZ666881 OM_Ba022
c	12	33.2	40.5	1077	3	BQ649061	BQ649061 AGENCOURT
	13	33.2	40.5	1761	3	BM808747	BM808747 AGENCOURT
	14	33	40.2	485	5	CD893097	CD893097 G118.122N
	15	33	40.2	538	4	CA680753	CA680753 wlm24.pk0
	16	33	40.2	579	4	CA632959	CA632959 wle1n.pk0
	17	33	40.2	641	5	CD926836	CD926836 GR45.100C
c	18	33	40.2	837	14	CT231335	CT231335 Sus scrofa
c	19	33	40.2	1119	5	CK215573	CK215573 FGAS02753
c	20	32.8	40.0	704	8	CO959189	CO959189 AGENCOURT
	21	32.8	40.0	795	14	AG310060	AG310060 Mus muscu
c	22	32.8	40.0	859	14	AG282470	AG282470 Mus muscu
	23	32.8	40.0	967	14	CNS00IYE	AL075395 Drosophil
c	24	32.6	39.8	468	14	CNS03ZNE	AL267827 Tetraodon
	25	32.6	39.8	1116	13	CL471067	CL471067 SAIL_155_
c	26	32.4	39.5	634	13	CZ615527	CZ615527 OM_Ba014
c	27	32.4	39.5	828	2	BG781046	BG781046 SEAUMC001
c	28	32.4	39.5	839	13	CW673918	CW673918 OP_Ba006
c	29	32.4	39.5	851	2	BI958166	BI958166 HVSMEn001
c	30	32.4	39.5	900	7	BB901768	BB901768 BB901768
	31	32.4	39.5	1026	3	BU900073	BU900073 AGENCOURT
	32	32.4	39.5	1053	13	CL482318	CL482318 SAIL_359_
c	33	32.2	39.3	831	14	AG395160	AG395160 Mus muscu
c	34	32.2	39.3	872	11	AZ190012	AZ190012 SP_1016_A
	35	32.2	39.3	873	5	CK154648	CK154648 FGAS03335
c	36	32.2	39.3	974	10	DV057041	DV057041 MONTH14_0
	37	32.2	39.3	1038	2	BG177276	BG177276 602314466
	38	32	39.0	407	5	CI291021	CI291021 CI291021
c	39	32	39.0	690	2	BJ273105	BJ273105 BJ273105
	40	32	39.0	760	9	DR165226	DR165226 RTPHOS1_3
	41	32	39.0	786	4	CB658925	CB658925 OSJNEc15G
c	42	32	39.0	809	13	CW944356	CW944356 TcB26.2_H
	43	32	39.0	1038	8	CX106365	CX106365 BI126E07
	44	32	39.0	1064	12	CL135995	CL135995 ISB1-107F
	45	32	39.0	1101	14	CNS01523	AL104901 Drosophil

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2923	TERT SAME promoter	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:36
L2	462	telomerase SAME promoter	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:37
L3	180	"human telomerase" SAME promoter	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:37
L4	183	hTERT SAME promoter	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:37
L5	87	"hTERT promoter"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:37
L6	8590	514/44.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:37
L7	62	I2 and I6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L8	20	I3 and I6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L9	21	I4 and I6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L10	13	I5 and I6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:39
L11	3553	536/24.1.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38

EAST Search History

L12	15	I2 and I11	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L13	8	I3 and I11	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L14	6	I4 and I11	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:38
L15	3	I5 and I11	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:39
L16	0	I10 and I15	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/09/18 09:39
S1	2	("6777203").PN.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/09/18 07:59
S2	3	("6610839").PN.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/09/18 08:00
S3	2	("6777203").PN.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/09/18 09:36